

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Escobedo, Jaime  
Quianjin, Hu  
Garcia, Pablo  
Williams, Lewis T.  
Kothakota, Srinivas
- (ii) TITLE OF THE INVENTION: Secreted Human Proteins
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Banner & Witcoff  
(B) STREET: 1001 G Street, NW  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20001
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 11-DEC-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/032757  
(B) FILING DATE: 11-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Kagan, Sarah A  
(B) REGISTRATION NUMBER: 32141  
(C) REFERENCE/DOCKET NUMBER: 2441.39505
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-508-9100  
(B) TELEFAX: 202-508-9299  
(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2063 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA	CGAGGCCTCA	GTCTTCCAGG	GCGGCGGTGG	GTGTCCGCTT	CTCTCTGCTC	60
TTCGACTGCA	CCGCACTCGC	GCGTGACCCT	GACTCCCCCT	AGTCAGCTCA	GCGGTGCTGC	120
CATGGCGTGG	CGGCGGCGCG	AAGCCGGCGT	CGGGGCTCGC	GGCGTGTTGG	CTCTGGCGTT	180
GCTCGCCCTG	GCCCTGTGCG	TGCCCCGGGC	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTGGA	GCGTCTCGGA	300
GAGTGGCCGC	TTCGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
GTGGGCGCCC	GGCGGAGACC	TCGAGGGCTG	CGCGCCCGAC	ACGCGCTTCT	TCGTGCCCGA	420
GCCCGGCGCC	CGAGGGGCGC	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
CAAGGACAAG	GTCGTGGTGG	CGGCGCGGAG	GAACGCCTCG	GCCGTCTGTC	TCTACAATGA	540
GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAACAGGAA	ATATAGTGGT	600
CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTTCATCA	GCGGTCAGTC	720
TGTGGTGTTC	GTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
ATTTTACTAT	ATACAGCGTT	TCCTATATAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
AAAAGAAACT	AAGAAAGTTA	TTGGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
GGGAATTGAT	GTTGATGCTG	AAAATTGTGC	AGTGTGTATT	GAAAAATTCA	AAGTAAAGGA	960
TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
TTTGGATCAC	CGAACATGTC	CAATGTGTAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
GGGAGAGCCT	GGGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
AGCTGCAAAT	TTGAGTCTAG	CCTTACCAGA	TGATGACGGA	AGTGATGACA	GCAGTCCACC	1200
ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
AGAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGACTCT	CGGCATGGAG	GACCCATCTC	1320
CTAGCACACG	TGCCCCACTGA	AGTGGCACCA	ACAGAAGTTT	GGCTTGAAC	AAAGGACATT	1380
TTATTTTTTT	TACTTTAGCA	CATAATTTGT	ATATTTGAAA	ATAATGTATA	TTATTTTACC	1440
TATTAGATTC	TGATTTGATA	TACAAAGGAC	TAAGATATTT	TCTTCTTGAA	GAGACTTTTC	1500
GATTAGTCCT	CATATATTTA	TCTACTAAAA	TAGAGTGTTC	ACCATGAACA	GTGTGTTGCT	1560
TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	TAAAGGACAG	GTGGTGTTC	1620
TAAATAATTG	GCTGCTATGG	TTCTGTAAAA	ACCAGTTAAT	TCTATTTTTC	AAGGTTTTTG	1680
GCAAAGCACA	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
ATCTCATGGG	CTTTCCCTGG	AGGAAAGGTT	TTTTTTGTTG	TTTTTTTTTT	AAGAAGTTGA	1800
AACTTGTAAG	CTGAGATGTC	TGTAGCTTTT	TTGCCCATCT	GTAGTGTATG	TGAAGATTTC	1860
AAAACCTGAG	AGCACTTTTT	CTTTGTTTAG	AATTATGAGA	AAGGCACTAG	ATGACTTTAG	1920
GATTTGCATT	TTTCCCTTTA	TTGCCTCATT	TCTTGTGACG	CCTTGTTGGG	GAGGGAAATC	1980
TGTTTATTTT	TTCTACAAA	TAAAAAGCTA	AGATTCTATA	TCGCAAAAAA	AAAAAAAAAA	2040
AAAAAAAAAA	TTCTGCGGC	CGC				2063

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCA	CGAGGTAGGC	AAGGGATAAA	AAGGCACCTA	AGGCCCTTTT	GCAATAAGAA	60
GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTTGG	GGAAGGTCCC	120

CGGCCCCC	AGCCCTCT	GGAGCCTC	CCTGGCTC	CCCACTCA	TCAGCCCT	180
GGCAGCCCC	CCACAGGG	CCTCTCCT	CTGGACAG	CTGCTGGT	CCCCGTCCC	240
TGGAGAAG	CAAGGCCA	GGTCGGCC	TGCTGCTG	CCTGCTGC	CTGCTGCAG	300
CGCCAGCAT	TCTGCAGC	GGTGGCTC	CAGGATCT	TCCAAGCT	CTTTATGGG	360
TCACTCAAC	AAAACAC	TCAGCCTC	TGGGTGGC	TGTGGAA	CCCTTCTC	420
TCTATTACC	CTGGGAGT	GCCATAGT	CCAACGTG	AATATCCT	AGACGGGG	480
ACTTCCACG	GCAGTCCT	TACAGCACA	GGCCGCC	CATTCACA	GATTATGT	540
ACCGGCTCT	TCTGAACT	ACAGAGGG	AGGAGAGC	CTTCTCAG	ATCTCAA	600
TGCGGAAG	GGACCAGT	GTGTATTT	GCCGAGTC	GCTGGAC	CGGAGATC	660
GGAGGCAG	GTTGCAGT	ATCAAGGG	CCAACTCA	CATCACC	GCTGTCAC	720
CCACCACC	CTGGAGGC	AGCAGACA	CCACCAT	CGGCCTC	GTCACAGA	780
GCAAAGGG	CTAGAATC	TGGCACCT	GTCTGGAC	TGCCATC	GTTGCATT	840
CTGTGCTGT	GCTCAAA	GTCAATTT	GA	CTCCTCCT	CTGTGGTG	900
GGAGAAGG	AGGTAGCA	GCGCCAAG	GTGACTTC	ACCAACAG	TGTGGGG	960
AGGGATGT	ATTAGCCCC	GAGGACGT	TGTGAGAC	GCTTGTG	CCTCCACA	1020
CGTTCCCC	TGGCAAGA	CATGGAG	ACCTGAG	CCTTTAA	GCAAAGCC	1080
AAGGCAGA	GAGGCTGG	CCCTGAAT	CCGAGTGG	GAGAGTT	TACAAGAG	1140
TTCATCCAG	AGCATCCA	CTGCAATG	ATAGGAAT	GGTCTGAA	CCACTGAA	1200
AAACCACT	CATTTGGG	CTGTTTAT	TAGCAGTG	AAGAGTTC	TTATCCTC	1260
CAAGGATG	AAAATACA	TTATTTTG	TACCATAA	AAAAA	AAAAATTC	1320
GCGGCCG						1328

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGG	CGAGGGCA	ATTCGATA	AAACCAAT	ACCTGTGT	GAGGAAAA	60
TCACTTTCT	CATTCACA	CCCAAGCG	AGGACCTT	AGTTGAGG	AGAGACG	120
AGCACCAGT	TTCCCTGG	AACCTGA	TCCCCCTC	CCAGCTG	ACCAGTG	180
ACATGACTG	GAGCCAGC	TTCCAGTC	GTA	ACTCGG	TCCAAAC	240
TGAAGATTG	CTGCGGGT	CTCCATCT	CG	AAAAGC	GAGA	300
ACTCAGCTC	AGTCAAAC	CCCTCTGT	GT	CCAAAG	AGGG	360
CTCATATGT	TGGGTCTC	GGCCCTGG	TG	GCAGCA	ACAC	420
TTGGGGGCA	TGATAAGC	CGTATGGA	AG	AAAAGG	CCCC	480
AGGGGCTG	CGACCTGG	CG	AG	AGCTCCT	CG	540
CAGTCAAGG	GCCGACCCC	AGCATCGC	CT	CGGACAT	CTC	600
AGCTGCGGC	AAGGCTGAG	CAGCTGGA	AA	CGGGAC	GAC	660
GGCAGATCC	GCTGACCAT	CGGCACAG	CT	CGCAGAGA	AA	720
ATGCCTGC	AAACCTCAT	GCCTTCTG	T	AAGACGG	CTC	780
ATTTATTAC	AGACAAGAG	CGTCAGGA	GG	AGGAAAA	AC	840
TAAATCCAG	GTTTGATCA	AGCTTTG	AT	TCAGTGT	TT	900
GAACGCTCG	CGTTGCCGT	AAGAACAG	TG	GCGGCTT	CCT	960
TTGGCAAAG	ATTGGTTG	CTGGCATC	TG	AAGAACT	GC	1020
ATGACCTCA	GGAAGATGG	ACGAGGCC	TC	AGGCGAT	GAC	1080
GCGTCTCTT	CAGCGTAG	CTCCACCT	CT	ACCCGGA	ACA	1140
AATGTTATTT	TTATAATTT	ATGGATTT	AG	TTATACAT	AC	1200
GTTGACATTT	CAGGCAAAT	TGGCCAAT	AT	TATCATTT	GAA	1260
CTAGGATTT	GCCAGTTCT	ACAACGTG	CA	G	TAGGGCG	1320
ACTCTGCTCA	GCTGTGTCC	TAGGAGTC	CG	ATGTGTCT	GT	1380
ATATATCACT	GAGGTATA	CT	AT	GCCATGTA	AATAGACT	1440

TGGTTTAAAT	TCAGAAAGGAA	ATAGATCAAG	GAAATATATA	TATTTTCTTC	TAAAACTTAT	1500
TAAATTCGTG	TGACAAATAA	TCATTTTCAT	CTTGGCAGCA	AAAAGTTCTC	AGTGACCTAT	1560
TTTGTGGTGT	TTCTTTTGA	AAAGAAAAGC	TGAAATATTA	TTAAATGCTA	GTATGTTTCT	1620
GCCCATTATG	AAAGATGAAA	TAAAGTATTC	AAAATATTAA	AAAAAAAAAA	AAAAAATTC	1680
TGCGGCCGC						1689

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCA	CGAGGAGCAG	ATCTGCAAGA	GTTTCGTTTA	TGGAGGCTGC	TTGGGCAACA	60
AGAACAACATA	CCTTCGGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTG	CAAGGTGGGC	120
CTTTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTTCCCCCA	GGGCCCCCTC	ATGGAAAGGC	180
GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
GCATCGACAG	TTTCTTGGAG	TGTGACGACA	CCCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
CTGCCTGTGA	AAAATACACG	AGTGGCTTTG	ACGAGCTCCA	GCGCATCCAT	TTCCCCAGCG	360
ACAAAGGGCA	CTGCGTGGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCGCGCT	420
GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCCTTTTAC	CTATGGTGGT	TGTTACGGCA	480
ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTGCGGGC	ATCTCCAAGA	540
AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
CTGTCGCAGT	GTTCTGGTGC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTTACTGCT	660
TCTTCAAGAA	CCAGAGAAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
CCAGCTCCAC	TGCTCTCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
GGCCCCCTCTG	AGCCTGGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
CAGAGGCCTG	GGCTGGGAAA	AACTTTGGAA	CCAGACTCTT	GCCTGTTTCC	CAGGCCCCACT	900
GTGCCTCAGA	GACCAGGGCT	CCAGCCCCCTC	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCCT	960
GAGAAAGCTC	AAAGGTTTGG	AAGGAGCAGA	AAACCCTTGG	GCCAGAAGTA	CCAGACTAGA	1020
TGGACCTGCC	TGCATAGGAG	TTTGGAGGAA	GTTGGAGTTT	TGTTTCCTCT	GTTCAAAGCT	1080
GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTCAGAC	CCTGGAGGCC	1140
CCAACCCCTGT	CCTCCCAGAC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
TTCCCTGTGT	AGTTTGTGCT	GTAAAGAGTT	GCTTTTGTGT	TATTTAATGC	TGTGGCATGG	1260
GTGAAGAGGA	GGGAAGAGG	CCTGTTTGGC	CTCTCTATCC	TCTCTTCTC	TTCCCCCAAG	1320
ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
GAAGCTCAGC	TGCATTCCGC	AGCCCCCACC	CCCAAGGTTT	TCCAACATCA	CAGCCCAGCC	1440
CGCCCACTGG	GTAATAAAAG	TGGTTTGTGG	AAAAAAAAAA	AAAAAAAAAA	AAGTCCTGCG	1500
GCCGC						1505

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTCTG	CCGCGCGGGG	TCGCGGCGGC	120

CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
GCGGCGCGCG	TGGCCCCTTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
TCCACGCTGG	AGGCGGTGCG	CGGCCGGCCC	TTCCGCGACG	TCCTCTCGCT	CAGCGACGGG	300
CCCCCGGGCG	CGGGCAGCGG	CGTGCCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
AGCAACCTGC	AGGAGAATCC	ATATGCTACA	CTGACCATGA	CTTTGGCACA	GACCAACTTC	420
TGCAAGAAAC	ATGGATTTGA	TCCACAAAGT	CCCCTTTGTG	TTCACATAAT	GCTGTCAGGA	480
ACTGTGACCA	AGGTGAATGA	AACAGAAAATG	GATATTGCAA	AGCATTCGTT	ATTCATTCGA	540
CACCCTGAGA	TGAAAACCTG	GCCTTCCAGC	CATAATTGGT	TCTTTGCTAA	GTTGAATATA	600
ACCAATATCT	GGGTCTGGA	CTACTTTGGT	GGACCAAAAA	TCGTGACACC	AGAAGAATAT	660
TATAATGTCA	CAGTTCAGTG	AAGCAGACTG	TGGTGAATTT	AGCAACACTT	ATGAAGTTTC	720
TTAAAGTGGC	TCATACACAC	TTAAAAGGCT	TAATGTTTCT	CTGGAAAGCG	TCCCAGAATA	780
TTAGCCAGTT	TTCTGTCACA	TGCTGGTTTG	TTTGCTTGCT	TGTTTACTTG	CTTGTTTACC	840
AATAGAGTTG	ACCTGTTATT	GGATTTCCCTG	GAAGATGTGG	TAGCTACTTT	TTTCCTATTT	900
TGAAGCCATT	TTCGTAGAGA	AATATCCTTC	ACTATAATCA	AATAAGTTTT	GTCCCATCAA	960
TTCCAAAGAT	GTTTCCAGTG	GTGCTCTTGA	AGAGGAATGA	GTACCAGTTT	TAAATTGCCC	1020
ATTGGCATT	GAAGGTAGTT	GAGTATGTGT	TCTTTATTCC	TAGAAGCCAC	TGTGCTTGGT	1080
AGAGTGCATC	ACTCACCACA	GCTGCCCTCT	GAGCTGCCTG	AGCCTGGTGC	AAAAGGATTG	1140
GCCCCCATTA	TGGTGCTTCT	GAATAAATCT	TGCCAAGATA	GACAAACAAT	GATGAAACTC	1200
AGATGGAGCT	TCTGACTCAT	GTTGATTTAT	GTCTCACAAT	CCTGGGTATT	GTTAATTCAA	1260
CATAGGGTGA	AACTATTTCT	GATAAAGAAC	TTTTGAAAAA	CTTTTATAC	TCTAAAGTGA	1320
TACTCAGAAC	AAAAGAAAGT	CATAAACTC	CTGAATTTAA	TTTCCCCACC	TAAGTCGAGA	1380
CAGTATTATC	AAAACACATG	TGCACACAGA	TTATTTTTTG	GCTCCAAAAC	TGGATTGCAA	1440
AAGAAAGAGG	AGAGATATTT	TGTGTGTTCC	TGGTATTCTT	TTATAAGTAA	AGTTACCCAG	1500
GCATGGACCA	GCTTCAGCCA	GGGACAAAAT	CCCCTCCCAA	ACCACTCTCC	ACAGCTTTTT	1560
AAAAATACTT	CTACTCTTAA	CAATTACCTA	AGGTTCCTTC	AAACCCCCC	AACTCTTAAT	1620
AGCTTCTAGT	GCTGCTACAA	TCTAAGTCAG	GTCACCAGAG	GGAAGAGAAC	ATGGCATTTAA	1680
AAGAATCACA	TCTTCAGAAG	AGAAGACACT	AATATTATTA	CCCATATACA	TGATTTCAGA	1740
AGATGACATA	AGATTCTCT	TAAAGAGGAA	ATGTCAGGAA	TCAAGCCACT	GAATCCTTAA	1800
AGAGAAAAGT	TGAATATGAG	TCATTGTGTC	TGAAAAGTGC	AAAGTGAAGT	TAAGTGAGAT	1860
CCAGCAAACA	GGTTCTGTTT	AAGAAAAATA	ATTTATACTA	AATTTAGTAA	AATGGACTTC	1920
TTATTCAAAG	CATCAATAAT	TAAAAGAATT	ATTTTAAAAA	AAAAAAAAAA	AAAAAAAAAA	1980
AAAAAAAAAT	TCCTGCGGCC	GC				2002

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGCA	CGAGGGCCAC	GACTCTGCTG	GCATTTCTTC	TATAGCCACT	GGAATCTGAT	60
CCTGATTGTC	TTCCACTACT	ACCAGGCCAT	CACCACTCCG	CCTGGGTACC	CACCCAGGG	120
CAGGAATGAT	ATCGCCACCG	TCTCATCTG	TAAGAAGTGC	ATTTACCCCA	AGCCAGCCCG	180
AACACACCAC	TGCAGCATCT	GCAACAGGTG	TGTGCTGAAG	ATGGATCACC	ACTGCCCTTG	240
GCTAAACAAT	TGTGTGGGCC	ACTATAACCA	TCGGTACTTC	TTCTCTTTCT	GCTTTTTTCAT	300
GACTCTGGGC	TGTGTCTACT	GCAGCTATGG	AAGTTGGGAC	CTTTTCCGGG	AGGCTTATGC	360
TGCCATTGAG	AAAATGAAAC	AGCTCGACAA	GAACAACTA	CAGGCGGTTG	CCAACCAGAC	420
TTATCACCAG	ACCCACCCAC	CCACCTTCTC	CTTTTCGAGAA	AGGATGACTC	ACAAGAGTCT	480
TGCTTACCTC	TGGTTCCTGT	GCAGTTCTGT	GGCACTTGCC	CTGGGTGCC	TAAGTGTATG	540
GCATGCTGTT	CTCATCAGTC	GAGGTGAGAC	TAGCATCGAA	AGGCACATCA	ACAAGAAGGA	600
GAGACGTCGG	CTACAGGCCA	AGGGCAGAGT	ATTTAGGAAT	CCTTACAAC	ACGGCTGCTT	660
GGACAACTGG	AAGGTATTCC	TGGGTGTGGA	TACAGGAAGG	CACTGGCTTA	CTCGGGTGCT	720
CTTACCTTCT	ACTCACTTGC	CCCATGGGAA	TGGAATGAGC	TGGGAGCCCC	CTCCCTGGGT	780

(2) INFORMATION FOR SEQ ID NO:7:

(A) LENGTH: 1573 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GAATTCGGCA	CGAGGAGCCT	GCCTTCATCT	AGGATGGCTC	CTCTGGGCAT	GCTGCTTGGG	60
CTGCTGATGG	CCGCTTGCTT	CACCTTCTGC	CTCAGTCATC	AGAACCTGAA	GGAGTTTGCC	120
CTGACCAACC	CAGAGAAGAG	CAGCACCAAA	GAAACAGAGA	GAAAAGAAAC	CAAAGCCGAG	180
GAGGAGCTGG	ATGCCGAAGT	CCTGGAGGTG	TTCACCCGA	CGCATGAGTG	GCAGGCCCTT	240
CAGCCAGGGC	AGGCTGTCCC	TGCAGGATCC	CACGTACGGC	TGAATCTTCA	GACTGGGGAA	300
AGAGAGGCAA	AACTCCAATA	TGAGGACAAG	TTCCGAAATA	ATTTGAAAGG	CAAAAGGCTG	360
GATATCAACA	CCAACACCTA	CACATCTCAG	GATCTCAAGA	GTGCACTGGC	AAAATTCAAG	420
GAGGGGGCAG	AGATGGAGAG	TTCAAAGGAA	GACAAGGCAA	GGCAGGCTGA	GGTAAAGCGG	480
CTCTTCCGCC	CCATTGAGGA	ACTGAAGAAA	GACTTTGATG	AGCTGAATGT	TGTCATTGAG	540
ACTGACATGC	AGATCATGGT	ACGGCTGATC	AACAAGTTCA	ATAGTTCCAG	CTCCAGTTTG	600
GAAGAGAAGA	TTGCTGCGCT	CTTTGATCTT	GAATATTATG	TCCATCAGAT	GGACAATGCG	660
CAGGACCTGC	TTTCTTTTGG	TGGTCTTCAA	GTGGTGATCA	ATGGGCTGAA	CAGCACAGAG	720
CCCCTCGTGA	AGGAGTATGC	TGCGTTTTGTG	CTGGGCGCTG	CTTTTTCAG	CAACCCCAAG	780
GTCCAGGTGG	AGGCCATCGA	AGGGGGAGCC	CTGCAGAAGC	TGCTGGTCAT	CCTGGCCACG	840
GAGCAGCCGC	TCACTGCAA	GAAGAAGGTC	CTGTTTGAC	TGTGCTCCCT	GCTGCGCCAC	900
TTCCCCATATG	CCCAGCGGA	GTTCTGAAG	CTCGGGGGGC	TGCAGGTCTT	GAGGACCTTG	960
GTGCAGGAGA	AGGGCAGGGA	GGTGCTCGCC	GTGCGCGTGG	TCACACTGCT	TACGACCTTG	1020
GTCACGGAGA	AGATGTTTCG	CGAGGAGGAG	GCTGAGCTGA	CCACGAGAT	GTCCCCAGAG	1080
AAGCTGCAGC	AGTATCGCCA	GGTACACCTC	CTGCCAGGCC	TGTGGGAACA	GGGCTGGTGC	1140
GAGATCACGG	CCCACCTCCT	GGCGCTGCCC	GAGCATGATG	CCCGTGAGAA	GGTGCTGCAG	1200
ACACTGGGCG	TCCTCCTGAC	CACCTGCCGG	GACCGCTACC	GTCAGGACCC	CCAGCTCGGC	1260
AGGACACTGG	CCAGCCTGCA	GGCTGAGTAC	CAGGTGCTGG	CCAGCCTGGA	GCTGCAGGAT	1320
GGTGAGGACG	AGGGCTACTT	CCAGGAGCTG	CTGGGCTCTG	TCAACAGCTT	GCTGAAGGAG	1380
CTGAGATGAG	GCCCCACCA	AGGACTGGAC	TGGGATGCCG	CTAGTGAGGC	TGAGGGGTGC	1440
CAGCGTGGGT	GGGCTTCTCA	GGCAGGAGGA	CATCTTGGCA	GTGCTGGCTT	GGCCATTAAA	1500
TGGA AACCTG	AAGGCCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1560
TTCCTGCGGC	CGC					1573

(A) LENGTH: 1185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGGGGGCT	TTAAGGGACA	GCTGAGCCGG	CAGGTGGCAG	ATCAGATGTG	60
GCAGGCTGGG	AAAAGACAAG	CCTCCAGGGC	CTTCAGCTTG	TACGCCAACA	TCGACATCCT	120
CAGACCTTAC	TTTGATGTGG	AGCCTGCTCA	GGTGCGAAGC	AGGCTCCTGG	AGTCCATGAT	180
CCCTATCAAG	ATGGTCAACT	TCCCCCAGAA	AATTGCAGGT	GAACCTCTATG	GACCTCTCAT	240
GCTGGTCTTC	ACTCTGGTTG	CTATCCTACT	CCATGGGATG	AAGACGTCTG	ACACTATTAT	300
CCGGGAGGGC	ACCCTGATGG	GCACAGCCAT	TGGCACCTGC	TTCGGCTACT	GGCTGGGAGT	360
CTCATCCTTC	ATTTACTTCC	TTGCCTACCT	GTGCAACGCC	CAGATCACCA	TGCTGCAGAT	420
GTTGGCACTG	CTGGGCTATG	GCCTCTTTGG	GCATTGCATT	GTCCTGTTCA	TCACCTATAA	480
TATCCACCTC	CACGCCCTCT	TCTACCTCTT	CTGGCTGTTG	GTGGGTGGAC	TGTCCACACT	540
GCGCATGGTA	GCAGTGTTGG	TGTCTCGGAC	CGTGGGCCCC	ACACAGCGGC	TGCTCCTCTG	600
TGGCACCCCTG	GCTGCCCTAC	ACATGCTCTT	CCTGCTCTAT	CTGCATTTTG	CCTACCACAA	660
AGTGGTAGAG	GGGATCCTGG	ACACACTGGA	GGGCCCCAAC	ATCCCGCCCA	TCCAGAGGGT	720
CCCCAGAGAC	ATCCCTGCCA	TGCTCCCTGC	TGCTCGGCTT	CCCACCACCG	TCCTCAACGC	780
CACAGCCAAA	GCTGTTGCGG	TGACCCTGCA	GTCACACTGA	CCCCACCTGA	AATTCTTGGC	840
CAGTCCTCTT	TCCCGCAGCT	GCAGAGAGGA	GGAAGACTAT	TAAAGGACAG	TCCTGATGAC	900
ATGTTTCGTA	GATGGGGTTT	GCAGCTGCCA	CTGAGCTGTA	GCTGCGTAAG	TACCTCCTTG	960
ATGCCTGTCTG	GCACTTCTGA	AAGGCACAAG	GCCAAGAACT	CCTGGCCAGG	ACTGCAAGGC	1020
TCTGCAGCCA	ATGCAGAAAA	TGGGTCAGCT	CCTTTTGAGAA	CCCCTCCCCA	CCTACCCCTT	1080
CCTTCCTCTT	TATCTCTCCC	ACATTGTCTT	GCTAAATATA	GACTTGGTAA	TTAAAATGTT	1140
GATTGAAGTC	TGGAATAAAA	AAAAAAAAAA	AATTCCTGCG	GCCGC		1185

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA	CGAGGCAAGC	CACCATCTTC	CTTCGGCCTG	CACCCCTTTA	AAGGCACCCA	60
GACCCCTCTG	GAAAAAGATG	AACTGAAGCC	CTTTGACATC	CTCCAGCCTA	AGGAGTACTT	120
CCAGCTCAGC	CGCCACACGG	TCATTAAGAT	GGGAAGTGAG	AACGAGGCCC	TGGATCTCTC	180
CATGAAGTCA	GTGCCCTGGC	TCAAGGCTGG	TGAAGTCAGT	CCCCCAATCT	TCCAGGAAGA	240
TGCAGCCCTA	GACCTGTCAG	TGGCAGCCCA	CCGGAAATCC	GAGCCTCCCC	CTGAGACACT	300
GTATGACAGT	GGTGCATCAG	TGGACAGCTC	AGGTCACACA	GTGATGGAGA	AACTTCCCAG	360
TGGCATGGAA	ATTTCTTTTG	CCCCTGCCAC	GTCCCATGAG	GCCCCAGCCA	TGATGGATAG	420
TCACATCAGC	AGCAGTGATG	CTGCTACCGA	GATGCTCAGC	CAGCCCAACC	ACCCAGCGG	480
CGAAGTCAAG	GCTGAAAATA	ACATTGAGAT	GGTGGGCGAG	TCCCAGGCGG	CCAAGGTCAT	540
TGTCTCTGTC	GAAGATGCTG	TGCCTACCAT	ATTCTGTGGC	AAGATCAAAG	GCCTCTCAGG	600
GGTGTCCACC	AAAAACTTCT	CCTTCAAAAAG	AGAAGACTCC	GTGCTTCAGG	GCTATGACAT	660
CAACAGCCAA	GGGGAAGAGT	CCATGGGAAA	TGCAGAGCCC	CTTAGGAAAC	CCATCAAAAA	720
CCGGAGCATA	AAGTTAAAGA	AAGTGAATC	CCAGGAAGTA	CACATGCTCC	CAATCAAAAA	780
ACAACGGCTG	GCCACCTTTT	TTCCAAGAAA	GTAAATAACG	GCTTTTTTAAA	ATTTGTATGA	840
TTATAATATG	GGGAAAGGTG	CATTGGTTTT	ATAAAAAGGC	ATTTAAAAACA	AATTATCTTT	900
GTTAATTATT	TTGGGGAGTA	GTTGGGAAAT	GGAAAGGTGA	ATTGGCTCTA	GAGGCCCTGT	960
ATGCTAGTAT	CATTTTCTTT	TTTAATTTTT	GACTTTTCAC	AAATGAGTAA	ATAAGAGCAA	1020
CCTATTTTTT	AAGCAGATTG	CACATTTTTT	GCAGCTTTAA	TGGAATATTG	GGTGAATTAG	1080
AGGGGTAAAA	AAAGCTATTT	TCATTGCCAC	AAAGTGCTTT	GATGATGTAA	TACCTAATAA	1140
AGGGTAGGAT	GAATATTTCA	CAATAAATGT	TTGTTTGCAC	TAAAAAATAA	AAAAAATAA	1200
AAAAAATAA	AAATTCCTGC	GGCCGC				1226

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCA	CGAGGGCGCC	ATGGTGAAGG	TGACGTTCAA	CTCCGCTCTG	GCCCAGAAGG	60
AGGCCAAGAA	GGACGAGCCC	AAGAGCGGCG	AGGAGGCGCT	CATCATCCCC	CCCGACGCCG	120
TCGCGGTGGA	CTGCAAGGAC	CCAGATGATG	TGGTACCAGT	TGGCCAAAGA	AGAGCCTGGT	180
GTTGGTGCAT	GTGCTTTGGA	CTAGCATTTA	TGCTTGCAGG	TGTATTCTA	GGAGGAGCAT	240
ACTTGACAA	ATATTTTGCA	CTTCAACCAG	ATGACGTGTA	CTACTGTGGA	ATAAAGTACA	300
TCAAAGATGA	TGTCATCTTA	AATGAGCCCT	CTGCAGATGC	CCCAGCTGCT	CTCTACCAGA	360
CAATTGAAGA	AAATATTTAA	ATCTTTGAAG	AAGAAGAAGT	TGAATTTATC	AGTGTGCCTG	420
TCCCAGAGTT	TGCAGATAGT	GATCCTGCCA	ACATTGTTCA	TGACTTTAAC	AAGAACTTA	480
CAGCCTATTT	AGATCTTAAC	CTGGATAAGT	GCTATGTGAT	CCCTCTGAAC	ACTTCCATTG	540
TTATGCCACC	CAGAAACCTA	CTGGAGTTAC	TTATTAACAT	CAAGGCTGGA	ACCTATTTGC	600
CTCAGTCCTA	TCTGATTCAT	GAGCACATGG	TTATTACTGA	TCGCATTGAA	AACATTGATC	660
ACCTGGGTTT	CTTTATTTAT	CGACTGTGTC	ATGACAAGGA	AACTTACAAA	CTGCAACGCA	720
GAGAAACTAT	TAAAGGTATT	CAGAAACGTG	AAGCCAGCAA	TTGTTTCGCA	ATTCGGCATT	780
TTGAAAACAA	ATTTGCCGTG	GAACTTTTAA	TTTGTTCTTG	AACAGTCAAG	AAAAACATTA	840
TTGAGGAAAA	TTAATATCAC	AGCATAACCC	CACCCTTTAC	ATTTTGTTGC	AGTTGATTAT	900
TTTTTAAAGT	CTTCTTTCAT	GTAAGTAGCA	AACAGGGCTT	TACTATCTTT	TCATCTCATT	960
AATTCAATTA	AAACCATTAC	CTTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1020
AAAAAAAAAA	AAAAAATTCC	TGCGGCCGC				1049

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCGGCA	CGAGGGGAGA	ATACTTTTTT	CGATGCCTAC	TGGAGACTTT	GATTCGAAGC	60
CCAGTTGGGC	CGACCAGGTG	GAGGAGGAGG	GGGAGGACGA	CAAATGTGTC	ACCAGCGAGC	120
TCCTCAAGGG	GATCCCTCTG	GCCACAGGTG	ACACCAGCCC	AGAGCCAGAG	CTACTGCCGG	180
GAGCTCCACT	GCCGCCTCCC	AAGGAGGTCA	TCAACGGAAA	CATAAAGACA	GTGACAGAGT	240
ACAAGATAGA	TGAGGATGGC	AAGAAGTTCA	AGATTGTCCG	CACCTTCAGG	ATTGAGACCC	300
GGAAGGCTTC	AAAGGCTGTC	GCAAGGAGGA	AGAAGTGGAA	GAAAGTTCGGG	AACTCAGAGT	360
TTGACCCCCC	CGGACCCAAT	GTGGCCACCA	CCACTGTCAG	TGACGATGTC	TCTATGACGT	420
TCATCACCAG	CAAAGAGGAC	CTGAAGTGCC	AGGAGGAGGA	GGACCCTATG	AACAAATTCA	480
AGGGCCAGAA	GATCGTGTCC	TGCCGCATCT	GCAAGGGCGA	CCACTGGACC	ACCCGCTGCC	540
CCTACAAGGA	TACGCTGGGG	CCCATGCAGA	AGGAGCTGGC	CGAGCAGCTG	GGCCTGTCTA	600
CTGGCGAGAA	GGAGAAGCTG	CCGGGAGAGC	TAGAGCCGGT	GCAGGCCACG	CAGAACAAGA	660
CAGGGGAAGTA	TGTGCCGCCG	AGCCTGCGCG	ACGGGGCCAG	CCGCCGCGGG	GAGTCCATGC	720
AGCCCAACCG	CAGAGCCGAC	GACAACGCCA	CCATCCGTGT	CACCAACTTG	CGCAGAGGAC	780
ACGCGTGAGA	CCGACCTGCA	GGAGCTCTTC	CGGCCTTTTC	GCTCCATCTC	CCGCATCTAC	840
CTGGCTAAGG	ACAAGACCAC	TGGCCAATCC	AAGGGCTTTG	CCTTCATCAG	CTTCCACCGC	900



CGCGAGGATG	CTGCGCGTGC	CATTGCCGGG	GTGTCCGGCT	TTGGCTACGA	CCACCTCATC	960
CTCAACGTCG	AGTGGGCCAA	GCCGTCCACC	AACTAAGCCA	GCTGCCACTG	TGTACTCGGT	1020
CCGGGACCCT	TGGCGACAGA	AGACAGCCTC	CGAGAGCGCG	GGCTCCAAGG	GCAATAAAGC	1080
AGCTCCACTC	TCAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1140
GC						1142

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCGGCA	CGAGGGAAAC	ATGGCGGTAG	GCTGGGACCA	TAACACAAGC	ATGACTATAT	60
GAAGGAAGAG	GAAGGTTTT	CTGAAGATGA	GGCGACTGAA	TCGGAAGAAA	ACTTTAAGTT	120
TGGTAAAGA	GTTGGATGCC	TTCCGAAGG	TTCTGAGAG	CTATGTAGAG	ACTTCAGCCA	180
GTGGAGGTAC	AGTTTCTCTA	ATAGCATTTA	CAACTATGGC	TTTATTAACC	ATAATGGAAT	240
TCTCAGTATA	TCAAGATACA	TGGATGAAGT	ATGAATACGA	AGTAGACAAG	GATTTTTCTA	300
GCAAATTAAG	AATTAATATA	GATATTACTG	TTGCCATGAA	GTGTCAATAT	GTTGGAGCGG	360
ATGTATTGGA	TTTAGCAGAA	ACAATGGTTG	CATCTGCAGA	TGGTTAGTT	TATGAACCAA	420
CAGTATTTGA	TCTTTCACCA	CAGCAGAAAG	AGTGGCAGAG	GATGCTGCAG	CTGATTCAGA	480
GTAGGCTACA	AGAAGAGCAT	TCACCTCAAG	ATGTGATATT	TAAAAGTGCT	TTTAAAAGTA	540
CATCAACAGC	TCTTCCACCA	AGAGAAGATG	ATTCATCACA	GTCTCCAAAT	GCATGCAGAA	600
TTCATGGCCA	TCTATATGTC	AATAAAGTAG	CAGGGAATTT	TCACATAACA	GTGGGCAAGG	660
CAATTCACA	TCCTCGTGGT	CATGCACATT	TGGCAGCACT	TGTCAACCAT	GAATCTTACA	720
ATTTTCTCA	TAGAATAGAT	CATTTGTCTT	TTGGAGAGCT	TGTTCCAGCA	ATTATTAATC	780
CTTTAGATGG	AACTGAAAAA	ATTGCTATAG	ATCACAACCA	GATGTTCCAA	TATTTTATTA	840
CAGTTGTGCC	AACAAAACCTA	CATACATATA	AAATATCAGC	AGACACCCAT	CAGTTTTCTG	900
TGACAGAAAG	GGAACGTATC	ATTAACCATG	CTGCAGGCAG	CCATGGAGTC	TCTGGGATAT	960
TTATGAAATA	TGATCTCAGT	TCTCTTATGG	TGACAGTTAC	TGAGGAGCAC	ATGCCATTCT	1020
GGCAGTTTTT	TGTAAGACTC	TGTGGTATTG	TTGGAGGAAT	CTTTTCAACA	ACAGGCATGT	1080
TACATGGAAT	TGGAAAATTT	ATAGTTGAAA	TAATTTGCTG	TCGTTTCAGA	CTTGGATCCT	1140
ATAAACCTGT	CAATTCTGTT	CCTTTTGAGG	ATGGCCACAC	AGACAACCAC	TTACCTCTTT	1200
TAGAAAATAA	TACACATTAA	CACCTCCCGA	TTGAAGGAGA	AAAACTTTTT	GCCTGAGACA	1260
TAAAACCTTT	TTTAAATAAT	AAAATATTGT	GCAATATATT	CAAAGAAAAG	AAAACACAAA	1320
TAAGCAGAAA	ACATACTTAT	TTTAAAAAAG	AAAAAAAAGG	ATAAAAAAC	CCAACTGAA	1380
ATTCTATATA	CGTTGTGTCT	GTTACAAATG	TCGTAGAAGA	AATCATGCAG	CTAAACGATG	1440
AAGAAGCCCA	ACTGGAGTGT	TGCTTTGAAG	ATGACGCCTT	CTTATATTTT	CATAGCAAAT	1500
GGGTGGTATC	AAAATCAGAC	ATTGCTTCTT	GCTGATAAAA	AGCCTGAAGG	AAATAAGTGA	1560
AACTACATCT	ATGGGAAAAA	AAAAAACATT	GAGAAGTGCA	AATGTTGCA	TCCTTTTGTT	1620
TTTAAAAGAT	ATGATGTCAG	AATAAAATGT	GGAAAACATA	CGGAAAAAAA	AAAAAAAATA	1680
AAATTCCTGC	GGCCGC					1696

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCGGCA	CGAGGCGGCA	CGAGGCGGCA	CGAGGGTGGC	ATATCACGGC	CATGGGGTCT	60
CAGCATTCGG	CTGCTGCTCG	CCCCTCCTCC	TGCAGGCGAA	AGCAAGAAGA	TGACAGGGAC	120
GGTTTGCTGG	CTGAACGAGA	GCAGGAAGAA	GCCATTGCTC	AGTTCCCATA	TGTGGAATTC	180
ACCGGGAGAG	ATAGCATCAC	CTGTCTCACG	TGCCAGGGGA	CAGGCTACAT	TCCAACAGAG	240
CAAGTAAATG	AGTTGGTGGC	TTTGATCCCA	CACAGTGATC	AGAGATTGCG	CCCTCAGCGA	300
ACTAAGCAAT	ATGTCTCCTC	GTCCATCCTG	CTTTGTCTCC	TGGCATCTGG	TTTGGTGGTT	360
TTCTTCCTGT	TTCCGCATTC	AGTCCTTGTG	GATGATGACG	GCATCAAAGT	GGTGAAAGTC	420
ACATTTAATA	AGCAAGACTC	CCTTGTAATT	CTCACCATCA	TGGCCACCCT	GAAAATCAGG	480
AACTCCAAT	TCTACACGGT	GGCAGTGACC	AGCCTGTCCA	GCCAGATTCA	GTACATGAAC	540
ACAGTGGTCA	GTACATATGT	GACTIONAAC	GTCTCCCTTA	TTCCACCTCG	GAGTGAGCAA	600
CTGGTGAAAT	TTACCGGGAA	GGCCGAGATG	GGAGGACCGT	TTTCCTATGT	GACTTCTTTC	660
TGCACGGTAC	CTGAGATCCT	GGTGACAAC	ATAGTGATCT	TCATGCCAAC	TTCAGTGAAG	720
ATTTCATACA	TTGGCCTCAT	GACCCAGAGC	TCCTTGGAGA	CACATCACTA	TGTGGATTGT	780
GGAGGAAATT	CCACAGCTAT	TTAACAATG	CTATTGGTTC	TTCCACACAG	CGCCTGTAGA	840
AGAGAGCACA	GCATATGTTT	CCAAGGCTTG	AGTTCTGGAC	CTACCCCCAC	GTGGTGTAAG	900
CAGAGGAGGA	ATTGGTTCAC	TTAACTCCCA	GCAAACATCC	TCCTGCCACT	TAGGAGGAAA	960
CACCTCCCTA	TGGTACCATT	TATGTTTCTC	AGAACCAGCA	GAATCAGTGC	CTAGCCTGTG	1020
CCCAGCAAAT	AGTTGGCACT	CAATAAAGAT	TTGCAGAATT	TAAAAAAAAA	AAAAAAAAAA	1080
AAAAAAATTC	CTGCGGCCGC					1100

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCGGCA	CGAGGGTACC	TGCTTTTCTA	TTGCCTCTTT	GAAACAATGG	TCACGTGTTT	60
CCATGTTCCC	TACTCGGCTC	TCACCATGTT	CATCAGCACC	GAGCAGACTG	AGCGGGATTC	120
TGCCACCGCC	TATCGGATGA	CTGTGGAAGT	GCTGGGCACA	GTGCTGGGCA	CGGCGATCCA	180
GGGACAAATC	GTGGGCCAAG	CAGACACGCC	TTGTTTCCAG	GACCTCAATA	GCTCTACAGT	240
AGCTTCACAA	AGTGCCAACC	ATACACATGG	CACCACCTCA	CACAGGGAAA	CGCAAAAGGC	300
ATACCTGCTG	GCAGCGGGGG	TCATTGTCTG	TATCTATATA	ATCTGTGCTG	TCATCCTGAT	360
CCTGGGCGTG	CGGGAGCAGA	GAGAACCTTA	TGAAGCCAG	CAGTCTGAGC	CAATCGCCTA	420
CTTCCGGGGC	CTACGGCTGG	TCATGAGCCA	CGGCCCATAC	ATCAAACCTA	TTACTGGCTT	480
CCTCTTCACC	TCCTTGGCTT	TCATGCTGGT	GGAGGGGAAC	TTTGTCTTGT	TTTGCACCTA	540
CACCTTGGGC	TTCCGCAATG	AATTCCAGAA	TCTACTCCTG	GCCATCATGC	TCTCGGCCAC	600
TTTAACCATT	CCCATCTGGC	AGTGGTTCTT	GACCCGGTTT	GGCAAGAAGA	CAGCTGTATA	660
TGTTGGGATC	TCATCAGCAG	TGCCATTTCT	CATCTTGGTG	GCCCTCATGG	AGAGTAACCT	720
CATCATTACA	TATGCGGTAG	CTGTGGCAGC	TGGCATCAGT	GTGGCAGCTG	CCTTCTTACT	780
ACCCTGGTCC	ATGCTGCCTG	ATGTCATTGA	CGACTTCCAT	CTGAAGCAGC	CCCACTTCCA	840
TGGAACCGAG	CCCATCTTCT	TCTCCTTCTA	TGTCTTCTTC	ACCAAGTTTG	CCTCTGGAGT	900
GTCAGTGGGC	ATTTCTACCC	TCAGTCTGGA	CTTTGCAGGG	TACCAGACCC	GTGGCTGCTC	960
GCAGCCGGAA	CGTGTCAAGT	TTACACTGAA	CATGCTCGTG	ACCATGGCTC	CCATAGTTCT	1020
CATCCTGCTG	GGCCTGCTGC	TCTTCAAAAT	GTACCCCAT	GATGAGGAGA	GGCGGCGGCA	1080
GAATAAGAAG	GCCCTGCAGG	CACTGAGGGA	CGAGGCCAGC	AGCTCTGGCT	GCTCAGAAAC	1140
AGACTCCACA	GAGCTGGCTA	GCATCCTCTA	GGGCCCGCCA	CGTTGCCCGA	AGCCACCATG	1200
CAGAAGGCCA	CAGAAGGGAT	CAGGACCTGT	CTGCCGGCTT	GCTGAGCAGC	TGGACTGCAG	1260
GTGCTAGGAA	GGGAAGTGAA	GACTCAAGGA	GGTGGCCAG	GACACTTGCT	GTGCTCACTG	1320
TGGGGCCGGC	TGCTCTGTGG	CCTCCTGCCT	CCCCTCTGCC	TGCCTGTGGG	GCCAAGCCCT	1380
GGGGCTGCCA	CTGTGAATAT	GCCAAGGACT	GATCGGGCCT	AGCCCGGAAC	ACTAATGTAG	1440
AAACCTTTTT	TTTACAGAGC	CTAATTAATA	ACTTAATGAC	TGTGTACATA	GCAATGTGTG	1500

TGTATGTATA TGTCTGTGAG CTATTAATGT TATTAATTTT CATAAAAGCT GGAAAGCAAA 1560  
 AAAAAAAAAA AAAAATTCCT GCGGCCGC 1588

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGGCGGAA GTCCCGTCTC ACGGTTGCC TGGCAGCGCG CGAGGCTGGT 60  
 GAGTCGGCAG CCCTGTGGCA GCCGGCGGGC TGGTTTCCAT GGTTGCACGA TTAGGAACCA 120  
 CCAGCTGCTG CATCCCATGG CCAGGGGTGG CGTCCAGGTG GCAGAGCAGC TAGGAACGCA 180  
 AGGCCTGAAC CTGGGGGCCAG ACACCTGCT CTCCCGGCCA TGGTCAACGA CCCTCCAGTA 240  
 CCTGCCTTAC TGTGGGCCCA GGAGGTGGGC CAAGTCTTGG CAGGCCGTGC CCGCAGGCTG 300  
 CTGCTGCAGT TTGGGGTGCT CTTCTGCACC ATCCTCCTTT TGCTCTGGGT GTCTGTCTTC 360  
 CTCTATGGCT CCTTCTACTA TTCCTATATG CCGACAGTCA GCCACCTCAG CCCTGTGCAT 420  
 TTCTACTACA GGACCGACTG TGATTCCCTC ACCACCTCAC TCTGCTCCTT CCCTGTTGCC 480  
 AATGTCTCGC TGAATAAGGG TGGACGTGAT CGGGTGCTGA TGTATGGACA GCCGTATCGT 540  
 GTTACCTTAG AGCTTGAGCT GCCAGAGTCC CCTGTGAATC AAGATTTGGG CATGTTCTTG 600  
 GTCACCATT CTGCTACAC CAGAGGTGGC CGAATCATCT CCACTTCTTC GCGTTCGGTG 660  
 ATGCTGCATT ACCGCTCAGA CCTGCTCCAG ATGCTGGACA CACTGGTCTT CTCTAGCCTC 720  
 CTGCTATTTG GCTTTGCAGA GCAGAAGCAG CTGCTGGAGG TGGAACCTCTA CGCAGACTAT 780  
 AGAGAGAACT CGTACGTGCC GACCACTGGA GCGATCATTG AGATCCACAG CAAGCGCATC 840  
 CAGCTGTATG GAGCCTACCT CCGCATCCAC GCGCACTTCA CTGGGCTCAG ATACCTGCTA 900  
 TACAACTTCC CGATGACCTG CGCCTTCATA GGTGTTGCCA GCAACTTCAC CTTCTCAGC 960  
 GTCATCGTGC TCTTCAGCTA CATGCAGTGG GTGTGGGGGG GCATCTGGCC CCGACACCGC 1020  
 TTCTCTTTGC AGGTTAACAT CCGAAAAAGA GACAATTCCC GGAAGGAAGT CCAACGAAGG 1080  
 ATCTCTGCTC ATCAGCCAGG GCCTGAAGGC CAGGAGGAGT CAACTCCGCA ATCAGATGTT 1140  
 ACAGAGGATG GTGAGAGCCC TGAAGATCCC TCAGGGACAG AGGTCAGCTG TCCGAGGAGG 1200  
 AGAAACCAGA TCAGCAGCCC CTGAGCGGAG AAGAGGAGCT AGAGCCTGAG GCCAGTGATG 1260  
 GTTCAGGCTC CTGGGAAGAT GCAGCTTTGC TGACGGAGGC CAACCTGCCT GCTCCTGCTC 1320  
 CTGCTTCTGC TTCTGCCCTT GTCCTAGAGA CTCTGGGCAG CTCTGAACCT GCTGGGGGTG 1380  
 CTCTCCGACA GCGCCCCACC TGCTCTAGTT CCTGAAGAAA AGGGGCAGAC TCCTCACATT 1440  
 CCAGCACTTT CCCACCTGAC TCCTCTCCCC TCGTTTTTCC TTCAATAAAC TATTTTGTGT 1500  
 CAAAAAAAAA AAAAAAAAAA AATTCCTGCG GCCGC 1535

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCA CGAGGGCGGG CGCTACGGGC TTGACTCCCC CAAGGCCGAG GTCCGCGGCC 60  
 AGGTGCTGGC GCCGTGCCCC CTCCACGGAG TTGCTGATCA TCTGGGCTGT GATCCACAAA 120  
 CCCGGTTCTT TGTCCTCCTT AATATCAAAC AGTGGATTGC CTTGCTGCAG AGGGGAAACT 180  
 GCACGTTTAA AGAGAAAATA TCACGGGCCG CTTTCCACAA TGCAATTGCT GTAGTCATCT 240  
 ACAATAATAA ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GGAGATATTA 300

TTGCTGTCAT	GATAACAGAA	TTGAGGGGTA	AGGATATTTT	GAGTTATCTG	GAGAAAAACA	360
TCTCTGTACA	AATGACAATA	GCTGTTGGAA	CTCGAATGCC	ACCGAAGAAC	TTCAGCCGTG	420
GCTCTCTAGT	CTTCGTGTCA	ATATCCTTTA	TTGTTTTGAT	GATTATTTCT	TCAGCATGGC	480
TCATATTCTA	CTTCATTCAA	AAGATCAGGT	ACACAAATGC	ACGCGACAGG	AACCAGCGTC	540
GTCTCGGAGA	TGCAGCCAAG	AAAGCCATCA	GTAAATTGAC	AACCAGGACA	GTAAAGAAGG	600
GTGACAAGGA	AACTGACCCA	GACTTTGATC	ATTGTGCAGT	CTGCATAGAG	AGCTATAAGC	660
AGAATGATGT	CGTCCGAATT	CTCCCCTGCA	AGCATGTTTT	CCACAAATCC	TGCGTGATC	720
CCTGGCTTAG	TGAACATTGT	ACCTGTCCTA	TGTGCAAACT	TAATATATTG	AAGGCCCTGG	780
GAATTGTGCC	GAATTTGCCA	TGTACTGATA	ACGTAGCATT	CGATATGGAA	AGGCTCACCA	840
GAACCAAGC	TGTTAACCGA	AGATCAGCCC	TCGGCGACCT	CGCCGGCGAC	AACTCCCTTG	900
GCCTTGAGCC	ACTTCGAACT	TCGGGGATCT	CACCTCTTCC	TCAGGATGGG	GAGCTCACTC	960
CGAGAACAGG	AGAAATCAAC	ATTGCAGTAA	CAAAAGAATG	GTTTATTATT	GCCAGTTTTG	1020
GCCTCCTCAG	TGCCCTCACA	CTCTGCTACA	TGATCATCAG	AGCCACAGCT	AGCTTGAATG	1080
CTAATGAGGT	AGAATGGTTT	TGAAGAAGAA	AAAACCTGCT	TTCTGACTGA	TTTTGCCTTG	1140
AAGGAAAAAA	GAACCTATTT	TTGTGCATCA	TTTACCAATC	ATGCCACACA	AGCATTTATT	1200
TTTAGTACAT	TTTATTTTTT	CATAAAATTG	CTAATGCCAA	AGCTTTGTAT	TAAAAGAAAT	1260
AAATAATAAA	ATAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAT	TCCTGCGGCC	1320
GC						1322

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCA	CGAGGCCCTC	CCGCGCTCCC	GGGGCGCGCG	GGCCGCGCCC	CCGACGCCCT	60
ACATATACTC	AGGTGCGCCC	CACCTGTCCG	CCCGCACCTG	CTGGCTCACC	TCCGAGCCAC	120
CTCTGCTGCG	CACCGCAGCC	TCGGACCTAC	AGCCCAGGAT	ACTTTGGGAC	TTGCCGGCGC	180
TCAGAAACGC	GCCCAGACGG	CCCTCCACC	TTTTGTTTGC	CTAGGGTCGC	CGAGAGCGCC	240
CGGAGGGAAC	CGCCTGGCCT	TCGGGGACCA	CCAATTTTGT	CTGGAACCAC	CCTCCCGGCG	300
TATCCTACTC	CCTGTGCCGC	GAGGCCATCG	CTTCACTGGA	GGGGTCGATT	TGTGTGTAGT	360
TTGGTGACAA	GATTTGCATT	CACCTGGCCC	AAACCCTTTT	TGCTCTTTTG	GGTGACCGGA	420
AAACTCCACC	TCAAGTTTTT	TTTTGTGGGG	CTGCCCCCA	AGTGTCGTTT	GTTTTACTGT	480
AGGGTCTCCC	GCCCGGCGCC	CCAGTGTTT	TCTGAGGGCG	GAAATGGCCA	ATTCGGGCCT	540
GCAATTGCTG	GGCTTCTCCA	TGGCCCTGCT	GGGTGGGTG	GGTCTGGTGG	CCTGCACCGC	600
CATCCCGCAG	TGGCAGATGA	GCTCCTATGC	GGGTGACAAC	ATCATCACGG	CCCAGGCCAT	660
GTACAAGGGG	CTGTGGATGG	ACTGCGTCAC	GCAGAGCACG	GGGATGATGA	GCTGCAAAAT	720
GTACGACTCG	GTGCTCGCCC	TGTCCGCGGC	CTTGCAGGCC	ACTCGAGCCC	TAATGGTGGT	780
CTCCCTGGTG	CTGGGCTTCC	TGGCCATGTT	TGTGGCCACG	ATGGGCATGA	AGTGCACGCG	840
CTGTGGGGGA	GACGACAAAG	TGAAGAAGGC	CCGTATAGCC	ATGGGTGGAG	GCATAATTTT	900
CATCGTGGCA	GGTCTTGCCG	CCTTGGTAGC	TTGCTCCTGG	TATGGCCATC	AGATTGTCAC	960
AGACTTTTAT	AACCCTTTGA	TCCCTACCAA	CATTAAGTAT	GAGTTTGGCC	CTGCCATCTT	1020
TATTGGCTGG	GCAGGGTCTG	CCCTAGTCAT	CCTGGGAGGT	GCACTGCTCT	CCTGTTCCCTG	1080
TCCTGGGAAT	GAGAGCAAGG	CTGGGTACCG	TGCACCCCGC	TCTTACCCTA	AGTCCAACCTC	1140
TTCCAAGGAG	TATGTGTGAC	CTGGGATCTC	CTTGCCCCAG	CCTGACAGGC	TATGGGAGTG	1200
TCTAGATGGT	TGAAAGGGCC	TGGGGCTGAG	CTCAGCCTGT	GGGCAGGGTG	CCGGACAAAG	1260
GCCTCCTGGT	CACCTGTCC	CTGACTCCA	TGTATAGTCC	TCTTGGGTTG	GGGGTGGGGG	1320
GGTGCCGTTG	GTGGGAGAGA	CAAAAAGAGG	GAGAGTGTGC	TTTTTGTA	GTAAATAAAAA	1380
ATAAGTATTG	GGAAGCAGGC	TTTTTTCCCT	TCAGGGCCTC	TGCTTTCCTC	CCGTCCAGAT	1440
CCTTGCAGGG	AGCTTGGAAC	CTTAGTGCAC	CTACTTCAGT	TCAGAACACT	TAGCACCCCA	1500
CTGACTCCAC	TGACAATTGA	CTAAAAGATG	CAGGTGCTCG	TATCTCGACA	TTCATTCCCA	1560
CCCCCTCTT	ATTTAAATAG	CTACCAAAGT	ACTTCTTTTT	TAATAAAAAA	ATAAAGATTT	1620

TTATTAGGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680  
 AAAAAAAAAA AAAAAAAAAATT CCTGCGGCCG C 1711

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGCA CGAGGGCAGG TCCAGAGTAA AGTCACTGAA GAGTGGGAAGC GAGGAAGGAA 60  
 CAGGATGATT AGACCTCAGC TGCGGACCGC GGGGCTGGGA CGATGCCTCC TGCCGGGGCT 120  
 GCTGCTGCTC CTGGTGCCCG TCCTCTGGGC CGGGGCTGAA AAGCTACATA CCCAGCCCTC 180  
 CTGCCCCGCG GTCTGCCAGC CCACGCGCTG CCCGCGCTG CCCACCTGCG CGCTGGGGAC 240  
 CACGCCGGTG TTCGACCTGT GCCGCTGTTG CCGCGTCTGC CCCGCGGCCG AGCGTGAAGT 300  
 CTGCGGCGGG GCGCAGGGCC AACCGTGCGC CCCGGGGCTG CAGTGCCTCC AGCCGCTGCG 360  
 CCCCCGGTTC CCCAGCACCT GCGGTTGCCC GACGCTGGGA GGGGCCGTGT GCGGCAGCGA 420  
 CAGGCGCACC TACCCAGCA TGTGCGCGCT CCGGGCCGAA AACCGCGCCG CGCGCCGCCT 480  
 GGGCAAGGTC CCGGCCGTGC CTGTGCAGTG GGGGAAGTGC GGGGATACAG GGACCAGAAG 540  
 CGCAGGCCCG CTCAGGAGGA ATTACAATT CATCGCCGCG GTGGTGGAGA AGGTGGCGCC 600  
 ATCGGTGGTT CACGTGCAGC TGTGGGCGAG GTTACTTCAC GGCAGCAGGC TTGTTCTCTGT 660  
 GTACAGTGGC TCTGGGTTCA TAGTGTCTGA GGACGGGCTC ATTATTACCA ATGCCCATGT 720  
 TGTCAAGAAC CAGCAGTGGA TTGAGTGGT GCTCCAGAAT GGGGCCCGTT ATGAAGCTGT 780  
 TGTCAAGGAT ATTGACCTTA AATTGGATCT TGCGGTGATT AAGATTGAAT CAAATGCTGA 840  
 ACTTCCTGTA CTGATGCTGG GAAGATCATC TGACCTTCGG GCTGGAGAGT TTGTGGTGGC 900  
 TTTGGGCAGC CCATTTTCTC TGCAGAACAC AGCTACTGCA GGAATTGTCA GCACCAAACA 960  
 GCGAGGGGGC AAAGAACTGG GGATGAAGGA TTCAGATATG GACTACGTCC AGATTGATGC 1020  
 CACAATTAAC TATGGGAATT CTGGTGGTCC TCTGGTGAAC TTGGATGGTG ATGTGATTGG 1080  
 CGTCAATTCA TTGAGGGTGA CTGATGGAAT CTCCTTTGCA ATTCCTTCAG ATCGAGTTAG 1140  
 GCAGTTCTTG GCAGAATACC ATGAGCACCA GATGAAAGGA AAGGCGTTTT CAAATAAGAA 1200  
 ATATCTGGGT CTGCAAATGC TGTCCCTCAC TGTGCCCTT AGTGAAGAAT TGAAAATGCA 1260  
 TTATCCAGAT TTCCCTGATG TGAGTTCTGG GGTTCATGTA TGTAAGTGG TTGAAGGAAC 1320  
 AGCTGCTCAA AGCTCTGGAT TGAGAGATCA CGATGTAATT GTCAACATAA ATGGGAAACC 1380  
 TATTACTACT ACAACTGATG TTGTTAAAGC TCTTGACAGT GATTCCCTTT CCATGGCTGT 1440  
 TCTTCGGGGA AAAGATAATT TGCTCTGAC AGTCATACCT GAAACAATCA ATTAAATATC 1500  
 TTGTTTTTAA GTGGGATTAT CTAAAAAAA AAAAAAAAAA TTCCTGCGGC CGC 1553

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA CGAGGGGAGC CGCTCCCGGA GCGCGGCCGT AGAGGCTGCA ATCGCAGCCG 60  
 GGAGCCCGCA GCGCGCGCCC CGAGCCCGCC GCGGCCCTTC GAGGGCGCCC CAGGCCGCGC 120  
 CATGGTGAAG GTGACGTTCA ACTCCGCTCT GGCCAGAAAG GAGGCCAAGA AGGACGAGCC 180  
 CGAGAGCGGC GAGGAGGCGC TCATCATCCC CCCCAGCCG GTCGCGGTGG ACTGCAAGGA 240

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CCCAGATGAT GTGGTACCAG TTGGCCAAAG AAGAGCCTGG TGTGGTGCA TGTGCTTTGG 300
ACTAGCATTT ATGCTTGCAAG GTGTTATTCT AGGAGGAGCA TACTTGTACA AATATTTTGC 360
ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT 420
AAATGAGCCC TCTGCAGATG CCCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA 480
AATCTTTGAA GAAGAAGAAG TTGAATTTAT CAGTGTGCCT GTCCCAGAGT TTGCAGATAG 540
TGATCCTGCC AACATTGTTT ATGACTTTAA CAAGAACTT ACAGCCTATT TAGATCTTAA 600
CCTGGATAAG TGCTATGTGA TCCCTCTGAA CACTTCCATT GTTATGCCAC CCAGAAACCT 660
ACTGGAGTTA CTTATTAACA TCAAGGCTGG AACCTATTTG CCTCAGTCCT ATCTGATTCA 720
TGAGCACATG GTTATTACTG ATCGCATTGA AAACATTGAT CACCTGGGTT TCTTTATTTA 780
TCGACTGTGT CATGACAAGG AAACCTACAA ACTGCAACGC AGAGAAACTA TTAAAGGTAT 840
TCAGAAACGT GAAGCCAGCA ATTGTTTCGC AATTCCGCAT TTTGAAAACA AATTTGCCGT 900
GGAAACTTTA ATTTGTTCTT GAACAGTCAA GAAAACATT ATTGAGGAAA ATTAATATCA 960
CAGCATAACC CCACCCTTTA CATTTTGTGC AGTGATATTT TTTAAAGTCT CTTTCATGTA 1020
AGTAGCAAAC AGGGCTTTAC TATCTTTTCA TCTCATTAAT TCAATTAAAA CCATTACCTT 1080
AAAATTTTTT TCTTTCGAAG TGTGGTGCTT TTTATATTTG AATTAGTAAC TGTATGAAGT 1140
CATAGATAAT AGTACATGTC ACCTTAGGTA GTAGGAAGAA TTACAATTTT TTTAAATCAT 1200
TTATCTGGAT TTTTATGTTT TATTAGCATT TTCAAGAAGA CGGATTATCT AGAGAATAAT 1260
CATATATATG CATACGTAAA AATGGACCAC AGTGACTTAT TTGTAGTTGT TAGTTGCCCT 1320
GCTACCTAGT TTGTTAGTGC ATTTGAGCAC ACATTTTAAAT TTTCCTCTAA TTAATAATGTG 1380
CAGTATTTTC AGTGTCAAAT ATATTTAACT ATTTAGAGAA TGATTTCCAC CTTTATGTTT 1440
TAATATCCTA GGCATCTGCT GTAATAATAT TTTAGAAAAT GTTTGGAATT TAAGAAATAA 1500
CTTGTGTTAC TAATTTGTAT AACCATATC TGTGCAATGG AATATAAATA TCACAAAGTT 1560
GTTTAAAAAA AAAAAAAAAA AAATTCCTGC GGCCGC 1596

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Ala Trp Arg Arg Arg Glu Ala Gly Val Gly Ala Arg Gly Val Leu
 1           5           10           15
Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly
 20           25           30
Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp
 35           40           45
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe
 50           55           60
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro
 65           70           75           80
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe
 85           90           95
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu
 100          105          110
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala
 115          120          125
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly
 130          135          140
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val
 145          150          155          160
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln

```

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: None

Met	Asp	Lys	Gly	Ser	Ala	Gly	His	Pro	Gly	Gly	Val	Leu	Val	Trp	Gly
1				5					10					15	
Arg	Ser	Pro	Ala	Pro	Thr	Ala	Leu	Trp	Gly	Ala	Ser	Pro	Trp	Leu	Ser
			20					25					30		
Pro	Leu	Thr	Ser	Ala	Leu	Arg	Gln	Pro	Leu	His	Arg	Ala	Pro	Leu	Leu
		35					40					45			
Pro	Gly	Gln	Leu	Cys	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Lys	Asn	Lys	Ala
	50				55						60				
Met	Gly	Arg	Pro	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	
65				70					75					80	
Ala	Phe	Leu	Gln	Pro	Gly	Gly	Ser	Thr	Gly	Ser	Gly	Pro	Ser	Tyr	Leu
			85						90					95	
Tyr	Gly	Val	Thr	Gln	Pro	Lys	His	Leu	Ser	Ala	Ser	Met	Gly	Gly	Ser
			100					105					110		
Val	Glu	Ile	Pro	Phe	Ser	Phe	Tyr	Tyr	Pro	Trp	Glu	Leu	Ala	Ile	Val

```

      115      120      125
Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
  130      135      140
Phe Tyr Ser Thr Arg Pro Ser Ile His Lys Asp Tyr Val Asn Arg
  145      150      155      160
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
      165      170      175
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
      180      185      190
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
      195      200      205
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr Trp Arg
  210      215      220
Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
  225      230      235      240
Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
      245      250      255
Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
      260      265      270
Leu Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser
      275      280      285
Ser Asp Phe
  290

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Thr Val Ser Gln Arg Phe Gln Leu Ser Asn Ser Gly Pro Asn Ser
  1      5      10      15
Thr Ile Lys Met Lys Ile Ala Leu Arg Val Leu His Leu Glu Lys Arg
      20      25      30
Glu Arg Pro Pro Asp His Gln His Ser Ala Gln Val Lys Arg Pro Ser
      35      40      45
Val Ser Lys Glu Gly Arg Lys Thr Ser Ile Lys Ser His Met Ser Gly
      50      55      60
Ser Pro Gly Pro Gly Gly Ser Asn Thr Ala Pro Ser Thr Pro Val Ile
      65      70      75      80
Gly Gly Ser Asp Lys Pro Gly Met Glu Glu Lys Ala Gln Pro Pro Glu
      85      90      95
Ala Gly Pro Gln Gly Leu His Asp Leu Gly Arg Ser Ser Ser Ser Leu
      100      105      110
Leu Ala Ser Pro Gly His Ile Ser Val Lys Glu Pro Thr Pro Ser Ile
      115      120      125
Ala Ser Asp Ile Ser Leu Pro Ile Ala Thr Gln Glu Leu Arg Gln Arg
      130      135      140
Leu Arg Gln Leu Glu Asn Gly Thr Thr Leu Gly Gln Ser Pro Leu Gly
      145      150      155      160
Gln Ile Gln Leu Thr Ile Arg His Ser Ser Gln Arg Asn Lys Leu Ile

```

The above sequence is a representation of the amino acid sequence of the protein.



Val	Val	Val	His	Ala	Cys	Arg	Asn	Leu	Ile	Ala	Phe	Ser	Glu	Asp	Gly
			180					185					190		
Ser	Asp	Pro	Tyr	Val	Arg	Met	Tyr	Leu	Leu	Pro	Asp	Lys	Arg	Arg	Ser
		195					200					205			
Gly	Arg	Arg	Lys	Thr	His	Val	Ser	Lys	Lys	Thr	Leu	Asn	Pro	Val	Phe
	210					215					220				
Asp	Gln	Ser	Phe	Asp	Phe	Ser	Val	Ser	Leu	Pro	Glu	Val	Gln	Arg	Arg
225					230					235					240
Thr	Leu	Asp	Val	Ala	Val	Lys	Asn	Ser	Gly	Gly	Phe	Leu	Ser	Lys	Asp
			245						250					255	
Lys	Gly	Leu	Leu	Gly	Lys	Val	Leu	Val	Ala	Leu	Ala	Ser	Glu	Glu	Leu
		260						265					270		
Ala	Lys	Gly	Trp	Thr	Gln	Trp	Tyr	Asp	Leu	Thr	Glu	Asp	Gly	Thr	Arg
	275						280					285			
Pro	Gln	Ala	Met	Thr											
	290														

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Glu	Arg	Arg	His	Pro	Val	Cys	Ser	Gly	Thr	Cys	Gln	Pro	Thr	Gln
1				5					10					15	
Phe	Arg	Cys	Ser	Asn	Gly	Cys	Cys	Ile	Asp	Ser	Phe	Leu	Glu	Cys	Asp
			20					25				30			
Asp	Thr	Pro	Asn	Cys	Pro	Asp	Ala	Ser	Asp	Glu	Ala	Ala	Cys	Glu	Lys
		35					40					45			
Tyr	Thr	Ser	Gly	Phe	Asp	Glu	Leu	Gln	Arg	Ile	His	Phe	Pro	Ser	Asp
	50					55				60					
Lys	Gly	His	Cys	Val	Asp	Leu	Pro	Asp	Thr	Gly	Leu	Cys	Lys	Glu	Ser
65					70					75					80
Ile	Pro	Arg	Trp	Tyr	Tyr	Asn	Pro	Phe	Ser	Glu	His	Cys	Ala	Arg	Phe
				85					90					95	
Thr	Tyr	Gly	Gly	Cys	Tyr	Gly	Asn	Lys	Asn	Asn	Phe	Glu	Glu	Glu	Gln
		100						105					110		
Gln	Cys	Leu	Glu	Ser	Cys	Arg	Gly	Ile	Ser	Lys	Lys	Asp	Val	Phe	Gly
	115						120					125			
Leu	Arg	Arg	Glu	Ile	Pro	Ile	Pro	Ser	Thr	Gly	Ser	Val	Glu	Met	Ala
	130					135					140				
Val	Ala	Val	Phe	Leu	Val	Ile	Cys	Ile	Val	Val	Val	Val	Ala	Ile	Leu
145					150					155					160
Gly	Tyr	Cys	Phe	Phe	Lys	Asn	Gln	Arg	Lys	Asp	Phe	His	Gly	His	His
			165						170					175	
His	His	Pro	Pro	Thr	Pro	Ala	Ser	Ser	Thr	Val	Ser	Thr	Thr	Glu	
		180					185					190			
Asp	Thr	Glu	His	Leu	Val	Tyr	Asn	His	Thr	Thr	Arg	Pro	Leu		
	195						200					205			

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Ala Gly Leu Ser Arg Gly Ser Ala Arg Ala Leu Leu Ala Ala Leu
 1          5          10          15
Leu Ala Ser Thr Leu Leu Ala Leu Val Ser Pro Ala Arg Gly Arg
 20          25          30
Gly Gly Arg Asp His Gly Asp Trp Asp Glu Ala Ser Arg Leu Pro Pro
 35          40          45
Leu Pro Pro Arg Glu Asp Ala Ala Arg Val Ala Arg Phe Val Thr His
 50          55          60
Val Ser Asp Trp Gly Ala Leu Ala Thr Ile Ser Thr Leu Glu Ala Val
 65          70          75          80
Arg Gly Arg Pro Phe Ala Asp Val Leu Ser Leu Ser Asp Gly Pro Pro
 85          90          95
Gly Ala Gly Ser Gly Val Pro Tyr Phe Tyr Leu Ser Pro Leu Gln Leu
 100         105         110
Ser Val Ser Asn Leu Gln Glu Asn Pro Tyr Ala Thr Leu Thr Met Thr
 115         120         125
Leu Ala Gln Thr Asn Phe Cys Lys Lys His Gly Phe Asp Pro Gln Ser
 130         135         140
Pro Leu Cys Val His Ile Met Leu Ser Gly Thr Val Thr Lys Val Asn
 145         150         155         160
Glu Thr Glu Met Asp Ile Ala Lys His Ser Leu Phe Ile Arg His Pro
 165         170         175
Glu Met Lys Thr Trp Pro Ser Ser His Asn Trp Phe Phe Ala Lys Leu
 180         185         190
Asn Ile Thr Asn Ile Trp Val Leu Asp Tyr Phe Gly Gly Pro Lys Ile
 195         200         205
Val Thr Pro Glu Glu Tyr Tyr Asn Val Thr Val Gln
 210         215         220

```

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Asp His His Cys Pro Trp Leu Asn Asn Cys Val Gly His Tyr Asn
 1          5          10          15
His Arg Tyr Phe Phe Ser Phe Cys Phe Phe Met Thr Leu Gly Cys Val
 20          25          30

```

Tyr Cys Ser Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala  
 35 40 45  
 Ile Glu Lys Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala  
 50 55 60  
 Asn Gln Thr Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu  
 65 70 75 80  
 Arg Met Thr His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser  
 85 90 95  
 Val Ala Leu Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile  
 100 105 110  
 Ser Arg Gly Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg  
 115 120 125  
 Arg Arg Leu Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr  
 130 135 140  
 Gly Cys Leu Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg  
 145 150 155 160  
 His Trp Leu Thr Arg Val Leu Leu Pro Ser Thr His Leu Pro His Gly  
 165 170 175  
 Asn Gly Met Ser Trp Glu Pro Pro Pro Trp Val Thr Ala His Ser Ala  
 180 185 190  
 Ser Val Met Ala Val  
 195

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe  
 1 5 10 15  
 Thr Phe Cys Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn  
 20 25 30  
 Pro Glu Lys Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala  
 35 40 45  
 Glu Glu Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His  
 50 55 60  
 Glu Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His  
 65 70 75 80  
 Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr  
 85 90 95  
 Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn  
 100 105 110  
 Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe  
 115 120 125  
 Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln  
 130 135 140  
 Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp  
 145 150 155 160  
 Phe Asp Glu Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val  
 165 170 175

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 180 185 190  
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 195 200 205  
 Ala Gln Asp Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly  
 210 215 220  
 Leu Asn Ser Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu  
 225 230 235 240  
 Gly Ala Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu  
 245 250 255  
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 260 265 270  
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 275 280 285  
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 290 295 300  
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 Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg  
 370 375 380  
 Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp  
 385 390 395 400  
 Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln  
 405 410 415  
 Ala Glu Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp  
 420 425 430  
 Glu Gly Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys  
 435 440 445  
 Glu Leu Arg  
 450

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr  
 1 5 10 15  
 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln  
 20 25 30  
 Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn  
 35 40 45  
 Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val  
 50 55 60

```

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr
65          70          75          80
Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
          85          90          95
Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
          100          105          110
Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
          115          120          125
Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
          130          135          140
Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
145          150          155          160
Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
          165          170          175
Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
          180          185          190
Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
          195          200          205
Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
210          215          220
Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
225          230          235          240
Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His
          245          250

```

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Gly Ser Glu Asn Glu Ala Leu Asp Leu Ser Met Lys Ser Val Pro
1          5          10          15
Trp Leu Lys Ala Gly Glu Val Ser Pro Pro Ile Phe Gln Glu Asp Ala
          20          25          30
Ala Leu Asp Leu Ser Val Ala Ala His Arg Lys Ser Glu Pro Pro Pro
          35          40          45
Glu Thr Leu Tyr Asp Ser Gly Ala Ser Val Asp Ser Ser Gly His Thr
          50          55          60
Val Met Glu Lys Leu Pro Ser Gly Met Glu Ile Ser Phe Ala Pro Ala
65          70          75          80
Thr Ser His Glu Ala Pro Ala Met Met Asp Ser His Ile Ser Ser Ser
          85          90          95
Asp Ala Ala Thr Glu Met Leu Ser Gln Pro Asn His Pro Ser Gly Glu
          100          105          110
Val Lys Ala Glu Asn Asn Ile Glu Met Val Gly Glu Ser Gln Ala Ala
          115          120          125
Lys Val Ile Val Ser Val Glu Asp Ala Val Pro Thr Ile Phe Cys Gly
          130          135          140
Lys Ile Lys Gly Leu Ser Gly Val Ser Thr Lys Asn Phe Ser Phe Lys
145          150          155          160

```

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr

Arg	Glu	Asp	Ser	Val	Leu	Gln	Gly	Tyr	Asp	Ile	Asn	Ser	Gln	Gly	Glu
				165					170					175	
Glu	Ser	Met	Gly	Asn	Ala	Glu	Pro	Leu	Arg	Lys	Pro	Ile	Lys	Asn	Arg
			180					185					190		
Ser	Ile	Lys	Leu	Lys	Lys	Val	Asn	Ser	Gln	Glu	Val	His	Met	Leu	Pro
		195					200					205			
Ile	Lys	Lys	Gln	Arg	Leu	Ala	Thr	Phe	Phe	Pro	Arg	Lys			
	210					215					220				

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys
1				5					10					15	
Lys	Asp	Glu	Pro	Lys	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
			20					25					30		
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
		35					40					45			
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
	50				55						60				
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
	65				70				75					80	
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
			85					90						95	
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
		100					105						110		
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Glu	Val	Glu
	115						120					125			
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
	130					135					140				
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
	145				150					155				160	
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
			165					170						175	
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr
		180					185						190		
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
		195					200					205			
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
	210					215					220				
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
	225				230					235				240	
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
			245					250						255	
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
		260						265							

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Met Pro Thr Gly Asp Phe Asp Ser Lys Pro Ser Trp Ala Asp Gln Val
 1          5          10          15
Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr Ser Glu Leu Leu Lys
      20          25          30
Gly Ile Pro Leu Ala Thr Gly Asp Thr Ser Pro Glu Pro Glu Leu Leu
      35          40          45
Pro Gly Ala Pro Leu Pro Pro Lys Glu Val Ile Asn Gly Asn Ile
      50          55          60
Lys Thr Val Thr Glu Tyr Lys Ile Asp Glu Asp Gly Lys Lys Phe Lys
65          70          75          80
Ile Val Arg Thr Phe Arg Ile Glu Thr Arg Lys Ala Ser Lys Ala Val
      85          90          95
Ala Arg Arg Lys Asn Trp Lys Lys Phe Gly Asn Ser Glu Phe Asp Pro
      100          105          110
Pro Gly Pro Asn Val Ala Thr Thr Thr Val Ser Asp Asp Val Ser Met
      115          120          125
Thr Phe Ile Thr Ser Lys Glu Asp Leu Asn Cys Gln Glu Glu Glu Asp
      130          135          140
Pro Met Asn Lys Phe Lys Gly Gln Lys Ile Val Ser Cys Arg Ile Cys
145          150          155          160
Lys Gly Asp His Trp Thr Thr Arg Cys Pro Tyr Lys Asp Thr Leu Gly
      165          170          175
Pro Met Gln Lys Glu Leu Ala Glu Gln Leu Gly Leu Ser Thr Gly Glu
      180          185          190
Lys Glu Lys Leu Pro Gly Glu Leu Glu Pro Val Gln Ala Thr Gln Asn
      195          200          205
Lys Thr Gly Lys Tyr Val Pro Pro Ser Leu Arg Asp Gly Ala Ser Arg
      210          215          220
Arg Gly Glu Ser Met Gln Pro Asn Arg Arg Ala Asp Asp Asn Ala Thr
225          230          235          240
Ile Arg Val Thr Asn Leu Arg Arg Gly His Ala
      245          250

```

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu

1	5	10	15												
Asp	Ala	Phe	Pro	Lys	Val	Pro	Glu	Ser	Tyr	Val	Glu	Thr	Ser	Ala	Ser
	20							25					30		
Gly	Gly	Thr	Val	Ser	Leu	Ile	Ala	Phe	Thr	Thr	Met	Ala	Leu	Leu	Thr
	35						40					45			
Ile	Met	Glu	Phe	Ser	Val	Tyr	Gln	Asp	Thr	Trp	Met	Lys	Tyr	Glu	Tyr
	50					55					60				
Glu	Val	Asp	Lys	Asp	Phe	Ser	Ser	Lys	Leu	Arg	Ile	Asn	Ile	Asp	Ile
65					70					75				80	
Thr	Val	Ala	Met	Lys	Cys	Gln	Tyr	Val	Gly	Ala	Asp	Val	Leu	Asp	Leu
				85					90					95	
Ala	Glu	Thr	Met	Val	Ala	Ser	Ala	Asp	Gly	Leu	Val	Tyr	Glu	Pro	Thr
			100					105					110		
Val	Phe	Asp	Leu	Ser	Pro	Gln	Gln	Lys	Glu	Trp	Gln	Arg	Met	Leu	Gln
	115					120						125			
Leu	Ile	Gln	Ser	Arg	Leu	Gln	Glu	Glu	His	Ser	Leu	Gln	Asp	Val	Ile
	130					135					140				
Phe	Lys	Ser	Ala	Phe	Lys	Ser	Thr	Ser	Thr	Ala	Leu	Pro	Pro	Arg	Glu
145					150					155				160	
Asp	Asp	Ser	Ser	Gln	Ser	Pro	Asn	Ala	Cys	Arg	Ile	His	Gly	His	Leu
				165					170					175	
Tyr	Val	Asn	Lys	Val	Ala	Gly	Asn	Phe	His	Ile	Thr	Val	Gly	Lys	Ala
			180					185					190		
Ile	Pro	His	Pro	Arg	Gly	His	Ala	His	Leu	Ala	Ala	Leu	Val	Asn	His
	195					200						205			
Glu	Ser	Tyr	Asn	Phe	Ser	His	Arg	Ile	Asp	His	Leu	Ser	Phe	Gly	Glu
	210					215					220				
Leu	Val	Pro	Ala	Ile	Ile	Asn	Pro	Leu	Asp	Gly	Thr	Glu	Lys	Ile	Ala
225					230					235				240	
Ile	Asp	His	Asn	Gln	Met	Phe	Gln	Tyr	Phe	Ile	Thr	Val	Val	Pro	Thr
			245						250					255	
Lys	Leu	His	Thr	Tyr	Lys	Ile	Ser	Ala	Asp	Thr	His	Gln	Phe	Ser	Val
			260					265					270		
Thr	Glu	Arg	Glu	Arg	Ile	Ile	Asn	His	Ala	Ala	Gly	Ser	His	Gly	Val
	275						280					285			
Ser	Gly	Ile	Phe	Met	Lys	Tyr	Asp	Leu	Ser	Ser	Leu	Met	Val	Thr	Val
	290					295					300				
Thr	Glu	Glu	His	Met	Pro	Phe	Trp	Gln	Phe	Phe	Val	Arg	Leu	Cys	Gly
305					310					315				320	
Ile	Val	Gly	Gly	Ile	Phe	Ser	Thr	Thr	Gly	Met	Leu	His	Gly	Ile	Gly
			325						330					335	
Lys	Phe	Ile	Val	Glu	Ile	Ile	Cys	Cys	Arg	Phe	Arg	Leu	Gly	Ser	Tyr
			340					345					350		
Lys	Pro	Val	Asn	Ser	Val	Pro	Phe	Glu	Asp	Gly	His	Thr	Asp	Asn	His
		355					360					365			
Leu	Pro	Leu	Leu	Glu	Asn	Asn	Thr	His							
	370					375									

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg  
 1 5 10 15  
 Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu  
 20 25 30  
 Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser  
 35 40 45  
 Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln  
 50 55 60  
 Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg  
 65 70 75 80  
 Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu  
 85 90 95  
 Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu  
 100 105 110  
 Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln  
 115 120 125  
 Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn  
 130 135 140  
 Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln  
 145 150 155 160  
 Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu  
 165 170 175  
 Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu  
 180 185 190  
 Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu  
 195 200 205  
 Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile  
 210 215 220  
 Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr  
 225 230 235 240  
 Val Asp Cys Gly Gly Asn Ser Thr Ala Ile  
 245 250

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Val Thr Cys Phe His Val Pro Tyr Ser Ala Leu Thr Met Phe Ile  
 1 5 10 15  
 Ser Thr Glu Gln Thr Glu Arg Asp Ser Ala Thr Ala Tyr Arg Met Thr  
 20 25 30  
 Val Glu Val Leu Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile  
 35 40 45  
 Val Gly Gln Ala Asp Thr Pro Cys Phe Gln Asp Leu Asn Ser Ser Thr  
 50 55 60  
 Val Ala Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg

65                      70                      75                      80  
 Glu Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile  
                                  85                      90                      95  
 Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln Arg  
                                  100                      105                      110  
 Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe Arg Gly  
                                  115                      120                      125  
 Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu Ile Thr Gly  
                                  130                      135                      140  
 Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu Gly Asn Phe Val  
 145                                   150                      155                      160  
 Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn Glu Phe Gln Asn Leu  
                                  165                      170                      175  
 Leu Leu Ala Ile Met Leu Ser Ala Thr Leu Thr Ile Pro Ile Trp Gln  
                                  180                      185                      190  
 Trp Phe Leu Thr Arg Phe Gly Lys Lys Thr Ala Val Tyr Val Gly Ile  
                                  195                      200                      205  
 Ser Ser Ala Val Pro Phe Leu Ile Leu Val Ala Leu Met Glu Ser Asn  
                                  210                      215                      220  
 Leu Ile Ile Thr Tyr Ala Val Ala Val Ala Ala Gly Ile Ser Val Ala  
 225                                   230                      235                      240  
 Ala Ala Phe Leu Leu Pro Trp Ser Met Leu Pro Asp Val Ile Asp Asp  
                                  245                      250                      255  
 Phe His Leu Lys Gln Pro His Phe His Gly Thr Glu Pro Ile Phe Phe  
                                  260                      265                      270  
 Ser Phe Tyr Val Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly  
                                  275                      280                      285  
 Ile Ser Thr Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys  
                                  290                      295                      300  
 Ser Gln Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met  
 305                                   310                      315                      320  
 Ala Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Leu Phe Lys Met Tyr  
                                  325                      330                      335  
 Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln Ala  
                                  340                      345                      350  
 Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp Ser Thr  
                                  355                      360                      365  
 Glu Leu Ala Ser Ile Leu  
 370

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val  
 1                      5                      10                      15  
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly  
                                  20                      25                      30  
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu

```

      35              40              45
Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
  50              55              60
Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
  65              70              75              80
Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
      85              90              95
Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
      100              105              110
Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
      115              120              125
Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
      130              135              140
Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
      145              150              155              160
Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
      165              170              175
Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
      180              185              190
Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
      195              200              205
Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg
      210              215              220
Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala
      225              230              235              240
Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln
      245              250              255
Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val
      260              265              270
Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile
      275              280              285
Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln
      290              295              300
Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr
      305              310              315              320
Glu Val Ser Cys Pro Arg Arg Arg Asn Gln Ile Ser Ser Pro
      325              330

```

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu
  1              5              10              15
Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val
      20              25              30
Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser
      35              40              45
Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile

```

50		55		60
Ile Ser Ser Ala Trp	Leu Ile Phe Tyr Phe	Ile Gln Lys Ile Arg Tyr		
65	70	75	80	
Thr Asn Ala Arg Asp	Arg Asn Gln Arg Arg	Leu Gly Asp Ala Ala Lys		
	85	90	95	
Lys Ala Ile Ser Lys	Leu Thr Thr Arg Thr	Val Lys Lys Gly Asp Lys		
	100	105	110	
Glu Thr Asp Pro Asp	Phe Asp His Cys Ala	Val Cys Ile Glu Ser Tyr		
	115	120	125	
Lys Gln Asn Asp Val	Val Arg Ile Leu Pro	Cys Lys His Val Phe His		
	130	135	140	
Lys Ser Cys Val Asp	Pro Trp Leu Ser Glu	His Cys Thr Cys Pro Met		
	145	150	155	160
Cys Lys Leu Asn Ile	Leu Lys Ala Leu Gly	Ile Val Pro Asn Leu Pro		
	165	170	175	
Cys Thr Asp Asn Val	Ala Phe Asp Met Glu	Arg Leu Thr Arg Thr Gln		
	180	185	190	
Ala Val Asn Arg Arg	Ser Ala Leu Gly Asp	Leu Ala Gly Asp Asn Ser		
	195	200	205	
Leu Gly Leu Glu Pro	Leu Arg Thr Ser Gly	Ile Ser Pro Leu Pro Gln		
	210	215	220	
Asp Gly Glu Leu Thr	Pro Arg Thr Gly Glu	Ile Asn Ile Ala Val Thr		
	225	230	235	240
Lys Glu Trp Phe Ile	Ile Ala Ser Phe Gly	Leu Leu Ser Ala Leu Thr		
	245	250	255	
Leu Cys Tyr Met Ile	Ile Arg Ala Thr Ala	Ser Leu Asn Ala Asn Glu		
	260	265	270	
Val Glu Trp Phe				
	275			

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ala	Asn	Ser	Gly	Leu	Gln	Leu	Leu	Gly	Phe	Ser	Met	Ala	Leu	Leu
1				5					10					15	
Gly	Trp	Val	Gly	Leu	Val	Ala	Cys	Thr	Ala	Ile	Pro	Gln	Trp	Gln	Met
		20						25					30		
Ser	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Thr	Ala	Gln	Ala	Met	Tyr	Lys	
		35				40					45				
Gly	Leu	Trp	Met	Asp	Cys	Val	Thr	Gln	Ser	Thr	Gly	Met	Met	Ser	Cys
	50				55					60					
Lys	Met	Tyr	Asp	Ser	Val	Leu	Ala	Leu	Ser	Ala	Ala	Leu	Gln	Ala	Thr
65				70					75					80	
Arg	Ala	Leu	Met	Val	Val	Ser	Leu	Val	Leu	Gly	Phe	Leu	Ala	Met	Phe
			85					90					95		
Val	Ala	Thr	Met	Gly	Met	Lys	Cys	Thr	Arg	Cys	Gly	Gly	Asp	Asp	Lys
		100						105					110		
Val	Lys	Lys	Ala	Arg	Ile	Ala	Met	Gly	Gly	Gly	Ile	Ile	Phe	Ile	Val

Ala	Gly	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ser	Trp	Tyr	Gly	His	Gln	Ile
130							135					140			
Val	Thr	Asp	Phe	Tyr	Asn	Pro	Leu	Ile	Pro	Thr	Asn	Ile	Lys	Tyr	Glu
145					150					155					160
Phe	Gly	Pro	Ala	Ile	Phe	Ile	Gly	Trp	Ala	Gly	Ser	Ala	Leu	Val	Ile
				165					170					175	
Leu	Gly	Gly	Ala	Leu	Leu	Ser	Cys	Ser	Cys	Pro	Gly	Asn	Glu	Ser	Lys
			180					185				190			
Ala	Gly	Tyr	Arg	Ala	Pro	Arg	Ser	Tyr	Pro	Lys	Ser	Asn	Ser	Ser	Lys
		195					200					205			
Glu	Tyr														
210															

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ile	Arg	Pro	Gln	Leu	Arg	Thr	Ala	Gly	Leu	Gly	Arg	Cys	Leu	Leu
1				5					10					15	
Pro	Gly	Leu	Leu	Leu	Leu	Val	Pro	Val	Leu	Trp	Ala	Gly	Ala	Glu	
			20					25				30			
Lys	Leu	His	Thr	Gln	Pro	Ser	Cys	Pro	Ala	Val	Cys	Gln	Pro	Thr	Arg
		35					40					45			
Cys	Pro	Ala	Leu	Pro	Thr	Cys	Ala	Leu	Gly	Thr	Thr	Pro	Val	Phe	Asp
		50				55					60				
Leu	Cys	Arg	Cys	Cys	Arg	Val	Cys	Pro	Ala	Ala	Glu	Arg	Glu	Val	Cys
65					70					75					80
Gly	Gly	Ala	Gln	Gly	Gln	Pro	Cys	Ala	Pro	Gly	Leu	Gln	Cys	Leu	Gln
				85					90					95	
Pro	Leu	Arg	Pro	Gly	Phe	Pro	Ser	Thr	Cys	Gly	Cys	Pro	Thr	Leu	Gly
			100					105					110		
Gly	Ala	Val	Cys	Gly	Ser	Asp	Arg	Arg	Thr	Tyr	Pro	Ser	Met	Cys	Ala
		115					120					125			
Leu	Arg	Ala	Glu	Asn	Arg	Ala	Ala	Arg	Arg	Leu	Gly	Lys	Val	Pro	Ala
		130				135					140				
Val	Pro	Val	Gln	Trp	Gly	Asn	Cys	Gly	Asp	Thr	Gly	Thr	Arg	Ser	Ala
145					150					155					160
Gly	Pro	Leu	Arg	Arg	Asn	Tyr	Asn	Phe	Ile	Ala	Ala	Val	Val	Glu	Lys
				165					170					175	
Val	Ala	Pro	Ser	Val	Val	His	Val	Gln	Leu	Trp	Gly	Arg	Leu	Leu	His
			180					185					190		
Gly	Ser	Arg	Leu	Val	Pro	Val	Tyr	Ser	Gly	Ser	Gly	Phe	Ile	Val	Ser
		195					200					205			
Glu	Asp	Gly	Leu	Ile	Ile	Thr	Asn	Ala	His	Val	Val	Arg	Asn	Gln	Gln
		210				215					220				
Trp	Ile	Glu	Val	Val	Leu	Gln	Asn	Gly	Ala	Arg	Tyr	Glu	Ala	Val	Val
225					230					235					240
Lys	Asp	Ile	Asp	Leu	Lys	Leu	Asp	Leu	Ala	Val	Ile	Lys	Ile	Glu	Ser

(2) INFORMATION FOR SEQ ID NO:38:

(A) LENGTH: 266 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys
1				5					10					15	
Lys	Asp	Glu	Pro	Glu	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
			20					25					30		
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
			35				40					45			
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
						55					60				
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
65					70					75				80	
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
				85					90					95	
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
			100					105					110		
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Glu	Val	Glu

		115				120				125					
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
	130					135					140				
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
145					150					155				160	
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
			165						170					175	
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr
		180						185					190		
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
	195						200					205			
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
	210					215					220				
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
225					230					235				240	
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
			245					250						255	
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
			260					265							

115  
 130  
 145  
 165  
 180  
 195  
 210  
 225  
 245  
 260